



1 P E

Attorney's Office No.: 11145-023US1

IN THE UNITED STATES RECEIVING OFFICE

Applicant : Leif Andersson et al.

Art Unit : Unknown

Serial No. : 10/070,794

Examiner : Unknown

Filed : March 8, 2002

Title : VARIANTS OF THE GAMMA CHAIN OF AMPK, DNA SEQUENCES
ENCODING THE SAME, AND USES THEREOF

MAIL STOP PCT

Commissioner for Patents

P.O. Box 1450

Alexandria, VA 22313-1450

VERIFIED STATEMENT UNDER 37 CFR §1.821(f)

I, Judith A. Wasilkus, declare that I personally prepared the paper and the computer-readable copy of the Sequence Listing filed herewith for the above-identified application and that the content of both is the same.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of The United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: May 23, 2003

Judith A. Wasilkus
Judith A. Wasilkus

Fish & Richardson P.C., P.A.
60 South Sixth Street, Suite 3300
Minneapolis, MN 55402
(612) 335-5070 telephone
(612) 288-9696 facsimile

60142814.doc

CERTIFICATE OF MAILING BY EXPRESS MAIL

Express Mail Label No. EV342626111US

May 23, 2003
Date of Deposit

SEQUENCE LISTING

<110> ANDERSSON, Leif
LOOFT, Christian
KALM, Ernst
MILAN, Denis
ROBIC, Annie
ROGEL-GAILLARD, Claire
IANNUCCELLI, Nathalie
GELLIN, Joël
LE ROY, Pascale
CHARDON, Patrick

<120> VARIANTS OF THE GAMMA CHAIN OF AMPK, DNA SEQUENCES ENCODING
THE SAME, AND USES THEREOF

<130> 11145-023US1

<140> US 10/070,794

<141> 2002-03-08

<150> PCT/EP00/09896

<151> 2000-09-11

<150> EP 00401388.4

<151> 2000-05-18

<150> EP 99402236.3

<151> 1999-09-10

<160> 42

<210> 1

<211> 1867

<212> DNA

<213> Sus scrofa

<220>

<221> CDS

<222> (472) .. (1389)

<400> 1

ttcctagagc aaggagagag ccgttcatgg ccatcccgag ctgtaaccac cagctcagaa 60
agaagccatg gggaccaggg gaacaaggcc tctagatgga caaggcagga ggatgtagag 120
gaagggggggc ctccggggccc gaggggaaggt ccccgagcca ggccagttgc tgagtccacc 180
gggcaggagg ccacattccc caaggccaca cccttgggcc aagccgctcc cttggccgag 240
gtggacaacc ccccaacaga gcgggacatc ctccccctctg actgtgcagc ctcagcctcc 300
gactccaaca cagaccatct ggatctgggc atagagttct cagcctcggc ggcgtcgggg 360
gatgagcttg ggctggtgga agagaagcca gccccgtgcc catccccaga ggtgctgtta 420

cccaggctgg	gctgggatga	tgagctgcag	aagccggggg	cccaggctcta	c	atg	cac	477								
						Met	His									
						1										
ttc	atg	cag	gag	cac	acc	tgc	tac	gat	gcc	atg	gcg	acc	agc	tcc	aaa	525
Phe	Met	Gln	Glu	His	Thr	Cys	Tyr	Asp	Ala	Met	Ala	Thr	Ser	Ser	Lys	
		5					10					15				
ctg	gtc	atc	ttc	gac	acc	atg	ctg	gag	atc	aag	aag	gcc	ttc	ttt	gcc	573
Leu	Val	Ile	Phe	Asp	Thr	Met	Leu	Glu	Ile	Lys	Lys	Ala	Phe	Phe	Ala	
	20					25					30					
ctg	gtg	gcc	aac	ggc	gtc	cga	gcg	gca	cct	ttg	tgg	gac	agc	aag	aag	621
Leu	Val	Ala	Asn	Gly	Val	Arg	Ala	Ala	Pro	Leu	Trp	Asp	Ser	Lys	Lys	
	35				40					45					50	
cag	agc	ttc	gtg	ggg	atg	ctg	acc	atc	aca	gac	ttc	atc	ttg	gtg	ctg	669
Gln	Ser	Phe	Val	Gly	Met	Leu	Thr	Ile	Thr	Asp	Phe	Ile	Leu	Val	Leu	
				55					60					65		
cac	cgc	tat	tac	agg	tcc	ccc	ctg	gtc	cag	atc	tac	gag	att	gaa	gaa	717
His	Arg	Tyr	Tyr	Arg	Ser	Pro	Leu	Val	Gln	Ile	Tyr	Glu	Ile	Glu	Glu	
			70					75					80			
cat	aag	att	gag	acc	tgg	agg	gag	atc	tac	ctt	caa	ggc	tgc	ttc	aag	765
His	Lys	Ile	Glu	Thr	Trp	Arg	Glu	Ile	Tyr	Leu	Gln	Gly	Cys	Phe	Lys	
		85					90					95				
cct	ctg	gtc	tcc	atc	tct	ccc	aat	gac	agc	ctg	ttc	gaa	gct	gtc	tac	813
Pro	Leu	Val	Ser	Ile	Ser	Pro	Asn	Asp	Ser	Leu	Phe	Glu	Ala	Val	Tyr	
	100					105					110					
gcc	ctc	atc	aag	aac	cgg	atc	cac	cgc	ctg	ccg	gtc	ctg	gac	cct	gtc	861
Ala	Leu	Ile	Lys	Asn	Arg	Ile	His	Arg	Leu	Pro	Val	Leu	Asp	Pro	Val	
	115				120					125					130	
tcc	ggg	gct	gtg	ctc	cac	atc	ctc	aca	cat	aag	cgg	ctt	ctc	aag	ttc	909
Ser	Gly	Ala	Val	Leu	His	Ile	Leu	Thr	His	Lys	Arg	Leu	Leu	Lys	Phe	
				135					140					145		
ctg	cac	atc	ttt	ggc	acc	ctg	ctg	ccc	cgg	ccc	tcc	ttc	ctc	tac	cgc	957
Leu	His	Ile	Phe	Gly	Thr	Leu	Leu	Pro	Arg	Pro	Ser	Phe	Leu	Tyr	Arg	
			150					155					160			
acc	atc	caa	gat	ttg	ggc	atc	ggc	aca	ttc	cga	gac	ttg	gcc	gtg	gtg	1005
Thr	Ile	Gln	Asp	Leu	Gly	Ile	Gly	Thr	Phe	Arg	Asp	Leu	Ala	Val	Val	
		165				170						175				
ctg	gaa	acg	gcg	ccc	atc	ctg	acc	gca	ctg	gac	atc	ttc	gtg	gac	cgg	1053
Leu	Glu	Thr	Ala	Pro	Ile	Leu	Thr	Ala	Leu	Asp	Ile	Phe	Val	Asp	Arg	
	180					185					190					
cgt	gtg	tct	gcg	ctg	cct	gtg	gtc	aac	gaa	act	gga	cag	gta	gtg	ggc	1101
Arg	Val	Ser														

Phe Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser
35 40 45

Lys Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu
 50 55 60
 Val Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile
 65 70 75 80
 Glu Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys
 85 90 95
 Phe Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala
 100 105 110
 Val Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp
 115 120 125
 Pro Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu
 130 135 140
 Lys Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu
 145 150 155 160
 Tyr Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala
 165 170 175
 Val Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val
 180 185 190
 Asp Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val
 195 200 205
 Val Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln
 210 215 220
 Thr Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg
 225 230 235 240
 Thr Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu
 245 250 255
 Gly Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val
 260 265 270
 Leu Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp
 275 280 285
 Ile Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly
 290 295 300
 Ala
 305

<210> 3

<211> 2109

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (472)..(1389)

<400> 3

```

ttcctagagc aagaaaacag cagctcatgg ccatacaccag ctgtgaccag cagctcagaa 60
agaatccgtg ggaaacggag ggccaaagcc ttgagatgga caaggcagaa gtcggtggag 120
gaagggggagc caccaggtca gggggaaggt ccccggtcca ggccaactgc tgagtccacc 180
gggctggagg ccacattccc caagaccaca cccttggtc aagctgatcc tgccgggggtg 240
ggcactccac caacaggggtg ggactgcctc ccctctgact gtacagcctc agctgcaggc 300
tccagcacag atgatgtgga gctggccacg gagttcccag ccacagaggc ctgggagtgt 360
gagctagaag gcctgctgga agagaggcct gccctgtgcc tgtccccgca ggccccattt 420
cccaagctgg gctgggatga cgaactgcgg aaacccggcg cccagatcta c atg cgc 477
                                         Met Arg
                                         1

ttc atg cag gag cac acc tgc tac gat gcc atg gca act agc tcc aag 525
Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser Lys
      5              10              15

cta gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt gct 573
Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe Ala
      20              25              30

ctg gtg gcc aac ggt gtg cgg gca gcc cct cta tgg gac agc aag aag 621
Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys
      35              40              45              50

cag agc ttt gtg ggg atg ctg acc atc act gac ttc atc ctg gtg ctg 669
Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val Leu
      55              60              65

cat cgc tac tac agg tcc ccc ctg gtc cag atc tat gag att gaa caa 717
His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu Gln
      70              75              80

cat aag att gag acc tgg agg gag atc tac ctg caa ggc tgc ttc aag 765
His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys
      85              90              95

cct ctg gtc tcc atc tct cct aat gat agc ctg ttt gaa gct gtc tac 813
Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr
      100             105             110

acc ctc atc aag aac cgg atc cat cgc ctg cct gtt ctt gac ccg gtg 861
Thr Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro Val
      115             120             125             130

```

tca ggc aac gta ctc cac atc ctc aca cac aaa cgc ctg ctc aag ttc	909
Ser Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys Phe	
135 140 145	
ctg cac atc ttt ggt tcc ctg ctg ccc cgg ccc tcc ttc ctc tac cgc	957
Leu His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg	
150 155 160	
act atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gct gtg gtg	1005
Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val Val	
165 170 175	
ctg gag aca gca ccc atc ctg act gca ctg gac atc ttt gtg gac cgg	1053
Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp Arg	
180 185 190	
cgt gtg tct gca ctg cct gtg gtc aac gaa tgt ggt cag gtc gtg ggc	1101
Arg Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val Val Gly	
195 200 205 210	
ctc tat tcc cgc ttt gat gtg att cac ctg gct gcc cag caa acc tac	1149
Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr Tyr	
215 220 225	
aac cac ctg gac atg agt gtg gga gaa gcc ctg agg cag agg aca cta	1197
Asn His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr Leu	
230 235 240	
tgt ctg gag gga gtc ctt tcc tgc cag ccc cac gag agc ttg ggg gaa	1245
Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly Glu	
245 250 255	
gtg atc gac agg att gct cgg gag cag gta cac agg ctg gtg cta gtg	1293
Val Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu Val	
260 265 270	
gac gag acc cag cat ctc ttg ggc gtg gtc tcc ctc tcc gac atc ctt	1341
Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile Leu	
275 280 285 290	
cag gca ctg gtg ctc agc cct gct ggc atc gat gcc ctc ggg gcc tga	1389
Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala	
295 300 305	
gaagatctga gtcctcaatc ccaagccaac tgcacactgg aagccaatga aggaattgag	1449
aacagcttca tttccccaac cccaatttgc tgggttcagct atgattcagg cttcttcagc	1509
cttcacaaaat tgcctttgcc ttacttgtgc tcccagaacc cttcgggcat gccagtgca	1569
ccatgggatg atgaaattaa ggagaacagc tgagtcaagc ttggagggtcc ctgaaccaga	1629
ggcactagga ttaccccagg gccatctgtg ctccatgccc gcccatcccc ttgccgcctg	1689
actgggctgg atggccccag tgggtttagt cagggtttct ggattcctcg gtttctgggc	1749
tacctatggc ttcagccttc agctcctggg agtcccagct gttgttccca gcaacgtcgc	1809

cactgccctc ctactctcca ggctttgtca tttcaaggct gctgaaatgc tgcatttcag 1869
 gggccaccat ggagcagccg ttatttatag aactgcctgt tggaggtggg gagtcctccc 1929
 tccattcttg tccagaaaac tccttagctc tcgcagtga ccatgttctt agtctccagg 1989
 gatggatggc cttgtatatg gaccctgag aatgagcaat tgagaaaaca aaacaaaagg 2049
 aacaatccat gaacttagat tttattgggt tcactcaaaa tgctgcagtc atttgacctg 2109

<210> 4

<211> 305

<212> PRT

<213> Homo sapiens

<400> 4

Met Arg Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser
 1 5 10 15

Ser Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe
 20 25 30

Phe Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser
 35 40 45

Lys Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu
 50 55 60

Val Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile
 65 70 75 80

Glu Gln His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys
 85 90 95

Phe Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala
 100 105 110

Val Tyr Thr Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp
 115 120 125

Pro Val Ser Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu
 130 135 140

Lys Phe Leu His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu
 145 150 155 160

Tyr Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala
 165 170 175

Val Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val
 180 185 190

Asp Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val
 195 200 205

Val Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln
 210 215 220

Thr Tyr Asn His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg
 225 230 235 240

Thr Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu
 245 250 255

Gly Glu Val Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val
 260 265 270

Leu Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp
 275 280 285

Ile Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly
 290 295 300

Ala
 305

<210> 5
 <211> 20
 <212> DNA
 <213> Sus scrofa

<400> 5
 ggaatttcaa gtcagccaac 20

<210> 6
 <211> 20
 <212> DNA
 <213> Sus scrofa

<400> 6
 cttcaaaaga ccgtgctact 20

<210> 7
 <211> 20
 <212> DNA
 <213> Sus scrofa

<400> 7
 ctgggaacct ctatatgctg 20

<210> 8
 <211> 20
 <212> DNA
 <213> Sus scrofa

<400> 8

tagggaaata caaatcacag

20

<210> 9

<211> 20

<212> DNA

<213> Sus scrofa

<400> 9

ctccagctca caggatgaca

20

<210> 10

<211> 26

<212> DNA

<213> Sus scrofa

<400> 10

gtttctgcag ctttagcatc tattcc

26

<210> 11

<211> 20

<212> DNA

<213> Sus scrofa

<400> 11

gaagtatcct gggcttctga

20

<210> 12

<211> 26

<212> DNA

<213> Sus scrofa

<400> 12

gtttctccag gtttccagac atccac

26

<210> 13

<211> 20

<212> DNA

<213> Sus scrofa

<400> 13

gcttctgtct gcccctactt

20

<210> 14

<211> 26

<212> DNA

<213> Sus scrofa

<400> 14

gtttctaagt tctactgtaa gacacc

26

<210> 15
 <211> 20
 <212> DNA
 <213> Sus scrofa

<400> 15
 ccaagctgtg gtggctgaat 20

<210> 16
 <211> 20
 <212> DNA
 <213> Sus scrofa

<400> 16
 cagcacagca gtgccaccta 20

<210> 17
 <211> 19
 <212> DNA
 <213> Sus scrofa

<400> 17
 caaactcttc taggcgtgt 19

<210> 18
 <211> 26
 <212> DNA
 <213> Sus scrofa

<400> 18
 gtttctggaa cttccatatg ccatgg 26

<210> 19
 <211> 20
 <212> DNA
 <213> Sus scrofa

<400> 19
 aggggtggatg gtaggcttca 20

<210> 20
 <211> 20
 <212> DNA
 <213> Sus scrofa

<400> 20
 gtctcgctcc tgaaggaagt 20

<210> 21
 <211> 20
 <212> DNA

<213> Sus scrofa

<400> 21

agtcacgtgg ccatgctatc

20

<210> 22

<211> 20

<212> DNA

<213> Sus scrofa

<400> 22

ctcaactgga ttgagtcagt

20

<210> 23

<211> 20

<212> DNA

<213> Sus scrofa

<400> 23

ttggcgcaac tggtatttct

20

<210> 24

<211> 19

<212> DNA

<213> Sus scrofa

<400> 24

aggcaaagga agagcacag

19

<210> 25

<211> 18

<212> DNA

<213> Sus scrofa

<400> 25

agccgtgggc atcgttgg

18

<210> 26

<211> 21

<212> DNA

<213> Sus scrofa

<400> 26

agaaggagac agacagggcga

21

<210> 27

<211> 1873

<212> DNA

<213> Sus scrofa

<220>

<221> CDS

<222> (1)..(1395)

<400> 27

atg agc ttc cta gag caa gga gag agc cgt tca tgg cca tcc cga gct	48
Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala	
1 5 10 15	
gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc	96
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala	
20 25 30	
tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc	144
Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly	
35 40 45	
ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag	192
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln	
50 55 60	
gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg	240
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu	
65 70 75 80	
gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac	288
Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp	
85 90 95	
tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc	336
Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly	
100 105 110	
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg	384
Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val	
115 120 125	
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg	432
Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg	
130 135 140	
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg	480
Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met	
145 150 155 160	
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc	528
His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	
165 170 175	
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt	576
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	
180 185 190	
gcc ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag	624
Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys	
195 200 205	
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg	672

Lys	Gln	Ser	Phe	Val	Gly	Met	Leu	Thr	Ile	Thr	Asp	Phe	Ile	Leu	Val	
210						215					220					
ctg	cac	cgc	tat	tac	agg	tcc	ccc	ctg	gtc	cag	atc	tac	gag	att	gaa	720
Leu	His	Arg	Tyr	Tyr	Arg	Ser	Pro	Leu	Val	Gln	Ile	Tyr	Glu	Ile	Glu	
225					230					235					240	
gaa	cat	aag	att	gag	acc	tgg	agg	gag	atc	tac	ctt	caa	ggc	tgc	ttc	768
Glu	His	Lys	Ile	Glu	Thr	Trp	Arg	Glu	Ile	Tyr	Leu	Gln	Gly	Cys	Phe	
				245					250					255		
aag	cct	ctg	gtc	tcc	atc	tct	ccc	aat	gac	agc	ctg	ttc	gaa	gct	gtc	816
Lys	Pro	Leu	Val	Ser	Ile	Ser	Pro	Asn	Asp	Ser	Leu	Phe	Glu	Ala	Val	
			260					265					270			
tac	gcc	ctc	atc	aag	aac	cgg	atc	cac	cgc	ctg	ccg	gtc	ctg	gac	cct	864
Tyr	Ala	Leu	Ile	Lys	Asn	Arg	Ile	His	Arg	Leu	Pro	Val	Leu	Asp	Pro	
			275				280					285				
gtc	tcc	ggg	gct	gtg	ctc	cac	atc	ctc	aca	cat	aag	cgg	ctt	ctc	aag	912
Val	Ser	Gly	Ala	Val	Leu	His	Ile	Leu	Thr	His	Lys	Arg	Leu	Leu	Lys	
		290				295					300					
ttc	ctg	cac	atc	ttt	ggc	acc	ctg	ctg	ccc	cgg	ccc	tcc	ttc	ctc	tac	960
Phe	Leu	His	Ile	Phe	Gly	Thr	Leu	Leu	Pro	Arg	Pro	Ser	Phe	Leu	Tyr	
305					310					315					320	
cgc	acc	atc	caa	gat	ttg	ggc	atc	ggc	aca	ttc	cga	gac	ttg	gcc	gtg	1008
Arg	Thr	Ile	Gln	Asp	Leu	Gly	Ile	Gly	Thr	Phe	Arg	Asp	Leu	Ala	Val	
				325					330					335		
gtg	ctg	gaa	acg	gcg	ccc	atc	ctg	acc	gca	ctg	gac	atc	ttc	gtg	gac	1056
Val	Leu	Glu	Thr	Ala	Pro	Ile	Leu	Thr	Ala	Leu	Asp	Ile	Phe	Val	Asp	
			340					345					350			
cgg	cgt	gtg	tct	gcg	ctg	cct	gtg	gtc	aac	gaa	act	gga	cag	gta	gtg	1104
Arg	Arg	Val	Ser	Ala	Leu	Pro	Val	Val	Asn	Glu	Thr	Gly	Gln	Val	Val	
		355					360					365				
ggc	ctc	tac	tct	cgc	ttt	gat	gtg	atc	cac	ctg	gct	gcc	caa	caa	aca	1152
Gly	Leu	Tyr	Ser	Arg	Phe	Asp	Val	Ile	His	Leu	Ala	Ala	Gln	Gln	Thr	
		370				375					380					
tac	aac	cac	ctg	gac	atg	aat	gtg	gga	gaa	gcc	ctg	agg	cag	cgg	aca	1200
Tyr	Asn	His	Leu	Asp	Met	Asn	Val	Gly	Glu	Ala	Leu	Arg	Gln	Arg	Thr	
385					390					395					400	
ctg	tgt	ctg	gaa	ggc	gtc	ctt	tcc	tgc	cag	ccc	cac	gag	acc	ttg	ggg	1248
Leu	Cys	Leu	Glu	Gly	Val	Leu	Ser	Cys	Gln	Pro	His	Glu	Thr	Leu	Gly	
				405					410					415		
gaa	gtc	att	gac	cgg	att	gtc	cgg	gaa	cag	gtg	cac	cgc	ctg	gtg	ctc	1296
Glu	Val	Ile	Asp	Arg	Ile	Val	Arg	Glu	Gln	Val	His	Arg	Leu	Val	Leu	
			420					425					430			


```

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
      180                      185                      190
Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
      195                      200                      205
Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
      210                      215                      220
Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
      225                      230                      235                      240
Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
      245                      250                      255
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
      260                      265                      270
Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
      275                      280                      285
Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
      290                      295                      300
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
      305                      310                      315                      320
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
      325                      330                      335
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
      340                      345                      350
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
      355                      360                      365
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
      370                      375                      380
Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
      385                      390                      395                      400
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
      405                      410                      415
Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
      420                      425                      430
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
      435                      440                      445
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
      450                      455                      460

```

```

<210> 29
<211> 2115
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)..(1395)

```

```

<400> 29
atg agc ttc cta gag caa gaa aac agc agc tca tgg cca tca cca gct   48
Met Ser Phe Leu Glu Gln Glu Asn Ser Ser Ser Trp Pro Ser Pro Ala
  1                      5                      10                      15

gtg acc agc agc tca gaa aga atc cgt ggg aaa cgg agg gcc aaa gcc   96
Val Thr Ser Ser Ser Glu Arg Ile Arg Gly Lys Arg Arg Ala Lys Ala
      20                      25                      30

```


ttg aga tgg aca agg cag aag tcg gtg gag gaa ggg gag cca cca ggt	144
Leu Arg Trp Thr Arg Gln Lys Ser Val Glu Glu Gly Glu Pro Pro Gly	
35 40 45	
cag ggg gaa ggt ccc cgg tcc agg cca act gct gag tcc acc ggg ctg	192
Gln Gly Glu Gly Pro Arg Ser Arg Pro Thr Ala Glu Ser Thr Gly Leu	
50 55 60	
gag gcc aca ttc ccc aag acc aca ccc ttg gct caa gct gat cct gcc	240
Glu Ala Thr Phe Pro Lys Thr Thr Pro Leu Ala Gln Ala Asp Pro Ala	
65 70 75 80	
ggg gtg ggc act cca cca aca ggg tgg gac tgc ctc ccc tct gac tgt	288
Gly Val Gly Thr Pro Pro Thr Gly Trp Asp Cys Leu Pro Ser Asp Cys	
85 90 95	
aca gcc tca gct gca ggc tcc agc aca gat gat gtg gag ctg gcc acg	336
Thr Ala Ser Ala Ala Gly Ser Ser Thr Asp Asp Val Glu Leu Ala Thr	
100 105 110	
gag ttc cca gcc aca gag gcc tgg gag tgt gag cta gaa ggc ctg ctg	384
Glu Phe Pro Ala Thr Glu Ala Trp Glu Cys Glu Leu Glu Gly Leu Leu	
115 120 125	
gaa gag agg cct gcc ctg tgc ctg tcc ccg cag gcc cca ttt ccc aag	432
Glu Glu Arg Pro Ala Leu Cys Leu Ser Pro Gln Ala Pro Phe Pro Lys	
130 135 140	
ctg ggc tgg gat gac gaa ctg cgg aaa ccc ggc gcc cag atc tac atg	480
Leu Gly Trp Asp Asp Glu Leu Arg Lys Pro Gly Ala Gln Ile Tyr Met	
145 150 155 160	
cgc ttc atg cag gag cac acc tgc tac gat gcc atg gca act agc tcc	528
Arg Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	
165 170 175	
aag cta gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt	576
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	
180 185 190	
gct ctg gtg gcc aac ggt gtg cgg gca gcc cct cta tgg gac agc aag	624
Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys	
195 200 205	
aag cag agc ttt gtg ggg atg ctg acc atc act gac ttc atc ctg gtg	672
Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val	
210 215 220	
ctg cat cgc tac tac agg tcc ccc ctg gtc cag atc tat gag att gaa	720
Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	
225 230 235 240	
caa cat aag att gag acc tgg agg gag atc tac ctg caa ggc tgc ttc	768
Gln His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	
245 250 255	

aag cct ctg gtc tcc atc tct cct aat gat agc ctg ttt gaa gct gtc	816
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val	
260 265 270	
tac acc ctc atc aag aac cgg atc cat cgc ctg cct gtt ctt gac ccg	864
Tyr Thr Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro	
275 280 285	
gtg tca ggc aac gta ctc cac atc ctc aca cac aaa cgc ctg ctc aag	912
Val Ser Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys	
290 295 300	
ttc ctg cac atc ttt ggt tcc ctg ctg ccc cgg ccc tcc ttc ctc tac	960
Phe Leu His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu Tyr	
305 310 315 320	
cgc act atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gct gtg	1008
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val	
325 330 335	
gtg ctg gag aca gca ccc atc ctg act gca ctg gac atc ttt gtg gac	1056
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp	
340 345 350	
cgg cgt gtg tct gca ctg cct gtg gtc aac gaa tgt ggt cag gtc gtg	1104
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val Val	
355 360 365	
ggc ctc tat tcc cgc ttt gat gtg att cac ctg gct gcc cag caa acc	1152
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr	
370 375 380	
tac aac cac ctg gac atg agt gtg gga gaa gcc ctg agg cag agg aca	1200
Tyr Asn His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr	
385 390 395 400	
cta tgt ctg gag gga gtc ctt tcc tgc cag ccc cac gag agc ttg ggg	1248
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly	
405 410 415	
gaa gtg atc gac agg att gct cgg gag cag gta cac agg ctg gtg cta	1296
Glu Val Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu	
420 425 430	
gtg gac gag acc cag cat ctc ttg ggc gtg gtc tcc ctc tcc gac atc	1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile	
435 440 445	
ctt cag gca ctg gtg ctc agc cct gct ggc atc gat gcc ctc ggg gcc	1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala	
450 455 460	
tga gaagatctga gtctctcaatc ccaagccaac tgcacactgg aagccaatga	1445

aggaattgag aacagcttca tttccccaac cccaatttgc tggttcagct atgattcagg 1505
 cttcttcagc cttccaaaat tgcctttgcc ttacttgtgc tcccagaacc cttcgggcat 1565
 gccagtgca ccatgggatg atgaaattaa ggagaacagc tgagtcaagc ttggaggtcc 1625
 ctgaaccaga ggcactagga ttaccccagg gccatctgtg ctccatgccc gcccatcccc 1685
 ttgccgcctg actgggtcgg atggccccag tgggtttagt cagggcttct ggattcctcg 1745
 gtttctgggc tacctatggc ttcagccttc agtcctggg agtcccagct gttgttccca 1805
 gcaacgtcgc cactgccctc ctactctcca ggctttgtca tttcaaggct gctgaaatgc 1865
 tgcatttcag gggccaccat ggagcagccg ttatttatag aactgcctgt tggaggtggg 1925
 gagtccctcc tccattcttg tccagaaaaac tccttagctc tcgcagtgag ccatgttctt 1985
 agtctccagg gatggatggc cttgtatatg gaccctgag aatgagcaat tgagaaaaca 2045
 aaacaaaagg aacaatccat gaacttagat tttattgggt tcaactcaaaa tgctgcagtc 2105
 atttgacctg 2115

<210> 30
 <211> 464
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Ser Phe Leu Glu Gln Glu Asn Ser Ser Ser Trp Pro Ser Pro Ala
 1 5 10 15
 Val Thr Ser Ser Ser Glu Arg Ile Arg Gly Lys Arg Arg Ala Lys Ala
 20 25 30
 Leu Arg Trp Thr Arg Gln Lys Ser Val Glu Glu Gly Glu Pro Pro Gly
 35 40 45
 Gln Gly Glu Gly Pro Arg Ser Arg Pro Thr Ala Glu Ser Thr Gly Leu
 50 55 60
 Glu Ala Thr Phe Pro Lys Thr Thr Pro Leu Ala Gln Ala Asp Pro Ala
 65 70 75 80
 Gly Val Gly Thr Pro Pro Thr Gly Trp Asp Cys Leu Pro Ser Asp Cys
 85 90 95
 Thr Ala Ser Ala Ala Gly Ser Ser Thr Asp Asp Val Glu Leu Ala Thr
 100 105 110
 Glu Phe Pro Ala Thr Glu Ala Trp Glu Cys Glu Leu Glu Gly Leu Leu
 115 120 125
 Glu Glu Arg Pro Ala Leu Cys Leu Ser Pro Gln Ala Pro Phe Pro Lys
 130 135 140
 Leu Gly Trp Asp Asp Glu Leu Arg Lys Pro Gly Ala Gln Ile Tyr Met
 145 150 155 160
 Arg Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
 165 170 175
 Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
 180 185 190
 Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
 195 200 205

Lys	Gln	Ser	Phe	Val	Gly	Met	Leu	Thr	Ile	Thr	Asp	Phe	Ile	Leu	Val
210						215					220				
Leu	His	Arg	Tyr	Tyr	Arg	Ser	Pro	Leu	Val	Gln	Ile	Tyr	Glu	Ile	Glu
225					230					235					240
Gln	His	Lys	Ile	Glu	Thr	Trp	Arg	Glu	Ile	Tyr	Leu	Gln	Gly	Cys	Phe
			245					250						255	
Lys	Pro	Leu	Val	Ser	Ile	Ser	Pro	Asn	Asp	Ser	Leu	Phe	Glu	Ala	Val
		260				265						270			
Tyr	Thr	Leu	Ile	Lys	Asn	Arg	Ile	His	Arg	Leu	Pro	Val	Leu	Asp	Pro
	275				280						285				
Val	Ser	Gly	Asn	Val	Leu	His	Ile	Leu	Thr	His	Lys	Arg	Leu	Leu	Lys
290				295						300					
Phe	Leu	His	Ile	Phe	Gly	Ser	Leu	Leu	Pro	Arg	Pro	Ser	Phe	Leu	Tyr
305				310					315						320
Arg	Thr	Ile	Gln	Asp	Leu	Gly	Ile	Gly	Thr	Phe	Arg	Asp	Leu	Ala	Val
			325					330						335	
Val	Leu	Glu	Thr	Ala	Pro	Ile	Leu	Thr	Ala	Leu	Asp	Ile	Phe	Val	Asp
	340						345					350			
Arg	Arg	Val	Ser	Ala	Leu	Pro	Val	Val	Asn	Glu	Cys	Gly	Gln	Val	Val
	355					360					365				
Gly	Leu	Tyr	Ser	Arg	Phe	Asp	Val	Ile	His	Leu	Ala	Ala	Gln	Gln	Thr
370				375						380					
Tyr	Asn	His	Leu	Asp	Met	Ser	Val	Gly	Glu	Ala	Leu	Arg	Gln	Arg	Thr
385				390					395						400
Leu	Cys	Leu	Glu	Gly	Val	Leu	Ser	Cys	Gln	Pro	His	Glu	Ser	Leu	Gly
			405					410						415	
Glu	Val	Ile	Asp	Arg	Ile	Ala	Arg	Glu	Gln	Val	His	Arg	Leu	Val	Leu
	420						425					430			
Val	Asp	Glu	Thr	Gln	His	Leu	Leu	Gly	Val	Val	Ser	Leu	Ser	Asp	Ile
	435					440					445				
Leu	Gln	Ala	Leu	Val	Leu	Ser	Pro	Ala	Gly	Ile	Asp	Ala	Leu	Gly	Ala
450						455					460				

<210> 31
 <211> 2022
 <212> DNA
 <213> Sus scrofa

<400> 31
 atggagcttg ccgagctaga gcaggcactg cgcagggtcc cgggggtccc ggggggctgg 60
 gagctggagc aactgaggcc agagggcaga gggcccacca ctgcggatac tccctcctgg 120
 agcagcctcg ggggacctaa gcatcaagag atgagcttcc tagagcaagg agagagccgt 180
 tcatggccat cccgagctgt aaccaccagc tcagaaagaa gccatgggga ccagggggaac 240
 aaggcctcta gatggacaag gcaggaggat gtagaggaag gggggcctcc gggcccagg 300
 gaagggtccc agtccaggcc agttgctgag tccaccgggc aggaggccac attccccaag 360
 gccacaccct tggcccaagc cgctcccttg gccgaggtgg acaaccccc aacagagcgg 420
 gacatcctcc cctctgactg tgcagcctca gcctccgact ccaacacaga ccatctggat 480
 ctgggcatag agttctcagc ctcggcggcg tcgggggatg agcttgggct ggtggaagag 540
 aagccagccc cgtgccccca cccagagggt ctgttaccca ggctgggctg ggatgatgag 600
 ctgcagaagc cggggggcca ggtctacatg cacttcatgc aggagcacac ctgctacgat 660
 gccatggcga ccagctccaa actggtcatc ttcgacacca tgctggagat caagaaggcc 720
 ttctttgccc tgggtggcaa cggcggtccga gcggcacctt tgtgggacag caagaagcag 780
 agcttcgtgg ggatgctgac catcacagac ttcattcttg tgctgcaccg ctattacagg 840
 tccccctgg tccagatcta cgagattgaa gaacataaga ttgagacctg gagggagatc 900
 taccttcaag gctgcttcaa gcctctgggtc tccatctctc ccaatgacag cctgttcgaa 960
 gctgtctacg ccctcatcaa gaaccggatc caccgcctgc cggctctgga ccctgtctcc 1020

```

ggggctgtgc tccacatcct cacacataag cggcttctca agttcctgca catctttggc 1080
accctgctgc cccggccctc cttcctctac cgcaccatcc aagatttggg catcggcaca 1140
ttccgagact tggccgtggt gctggaaacg gcgcccaccc tgaccgcact ggacatcttc 1200
gtggaccggc gtgtgtctgc gctgcctgtg gtcaacgaaa ctggacaggt agtgggcctc 1260
tactctcgct ttgatgtgat ccacctggct gcccaacaaa catacaacca cctggacatg 1320
aatgtgggag aagccctgag gcagcggaca ctgtgtctgg aaggcgtcct ttcctgccag 1380
ccccacgaga ccttggggga agtcattgac cggattgtcc gggaacaggt gcaccgcctg 1440
gtgctcgtgg atgagaccca gcaccttctg ggcgtggtgt ccctctctga catccttcag 1500
gctctggtgc tcagccctgc tggaattgat gccctcgggg cctgagaacc ttggaacctt 1560
tgctctcagg ccacctggca cacctggaag ccagtgaagg gagccgtgga ctcagctctc 1620
acttcccctc agccccactt gctggtctgg ctcttgttca ggtaggctcc gcccggggcc 1680
cctggcctca gcatcagccc ctcagctctc ctgggcaccc agatctcaga ctggggcacc 1740
ctgaagatgg gagtggccca gcttatagct gagcagcctt gtgaaatcta ccagcatcaa 1800
gactcactgt gggaccactg ctttgtccca ttctcagctg aaatgatgga gggcctcata 1860
agaggggtgg acaggggcctg gagtagaggc cagatcagtg acgtgccttc aggacctccg 1920
gggagttaga gctgccctct ctcagttcag ttccccctg ctgagaatgt ccctggaagg 1980
aagccagtta ataaaccttg gttggatgga atttggagag tc 2022

```

<210> 32

<211> 514

<212> PRT

<213> Sus scrofa

<400> 32

```

Met Glu Leu Ala Glu Leu Glu Gln Ala Leu Arg Arg Val Pro Gly Ser
  1             5             10            15

```

```

Arg Gly Gly Trp Glu Leu Glu Gln Leu Arg Pro Glu Gly Arg Gly Pro
      20             25            30

```

```

Thr Thr Ala Asp Thr Pro Ser Trp Ser Ser Leu Gly Gly Pro Lys His
    35             40            45

```

```

Gln Glu Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser
    50             55            60

```

```

Arg Ala Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn
    65             70            75            80

```

```

Lys Ala Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro
      85             90            95

```

```

Pro Gly Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr
    100            105            110

```

```

Gly Gln Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala
    115            120            125

```

```

Pro Leu Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro
    130            135            140

```

```

Ser Asp Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp
    145            150            155            160

```

```

Leu Gly Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly
    165            170            175

```

Leu Val Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu
 180 185 190
 Pro Arg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val
 195 200 205
 Tyr Met His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr
 210 215 220
 Ser Ser Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala
 225 230 235 240
 Phe Phe Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp
 245 250 255
 Ser Lys Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile
 260 265 270
 Leu Val Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu
 275 280 285
 Ile Glu Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly
 290 295 300
 Cys Phe Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu
 305 310 315 320
 Ala Val Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu
 325 330 335
 Asp Pro Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu
 340 345 350
 Leu Lys Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe
 355 360 365
 Leu Tyr Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu
 370 375 380
 Ala Val Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe
 385 390 395 400
 Val Asp Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln
 405 410 415
 Val Val Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln
 420 425 430
 Gln Thr Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln
 435 440 445
 Arg Thr Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr
 450 455 460
 Leu Gly Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu
 465 470 475 480

Val Leu Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser
 485 490 495

Asp Ile Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu
 500 505 510

Gly Ala

<210> 33
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 33
 ggagcaaattg tgcagacaag 20

<210> 34
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 34
 cccacgaagc tctgcttctt 20

<210> 35
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 35
 tggccaacgg cgtcca 16

<210> 36
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 36
 ggccaacggc gtccg 15

<210> 37
 <211> 25
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 37

agcggcacct ttgtgaaaaa aaaaa

25

<210> 38

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 38

caaactcttc taggcgtgt

19

<210> 39

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 39

gtttctggaa cttccatatg ccatgg

26

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 40

gggaacgatt caccctcaac

20

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 41

agccccctct caccacgaa

20

<210> 42

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 42

aaaaaccaaa aaaaccgctc agcccctcct cacccacgaa

40